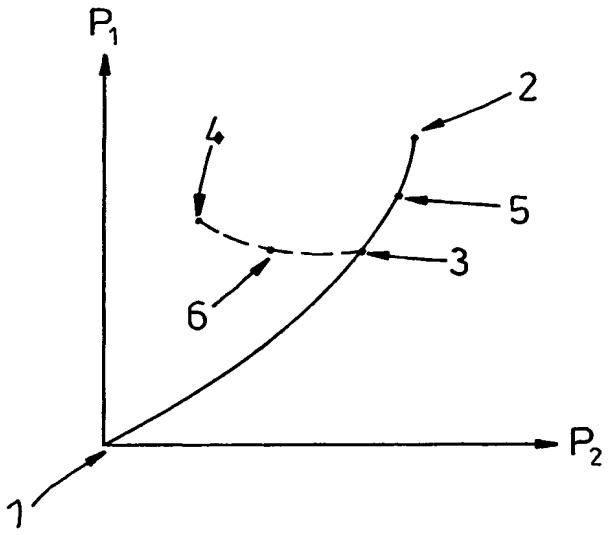

Fig. 1

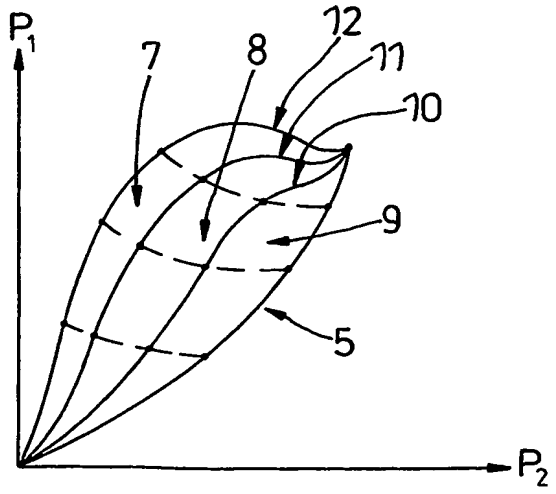

Fig. 2

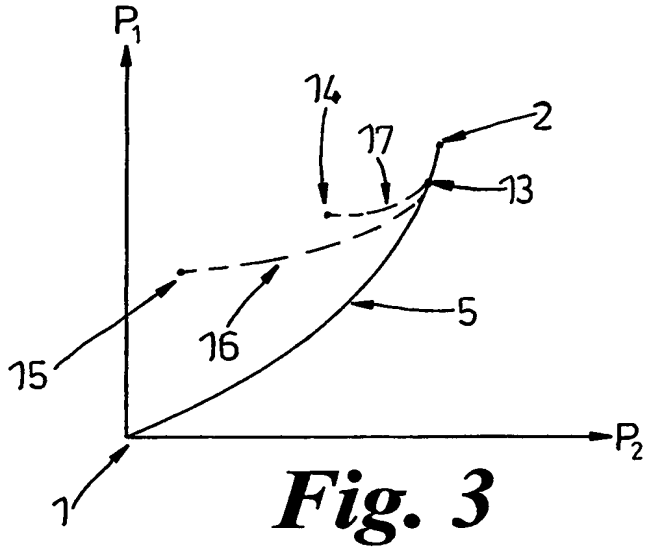

Fig. 3

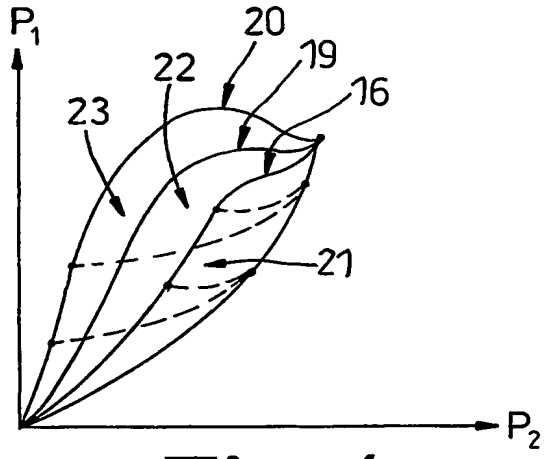

Fig. 4

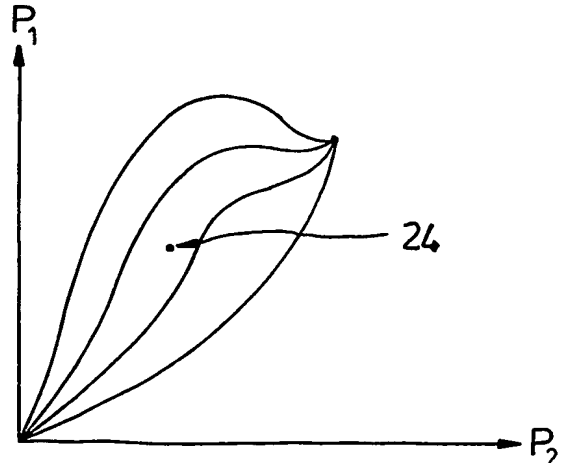

Fig. 5

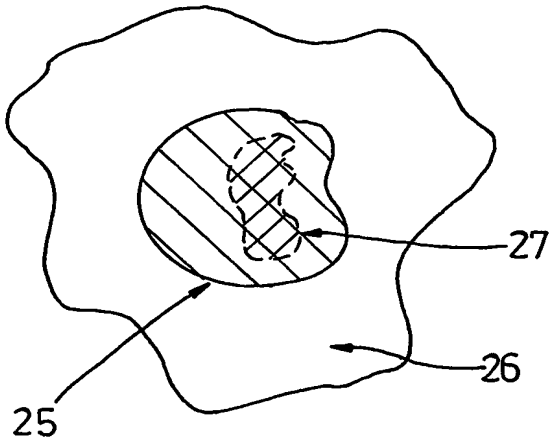

Fig. 6

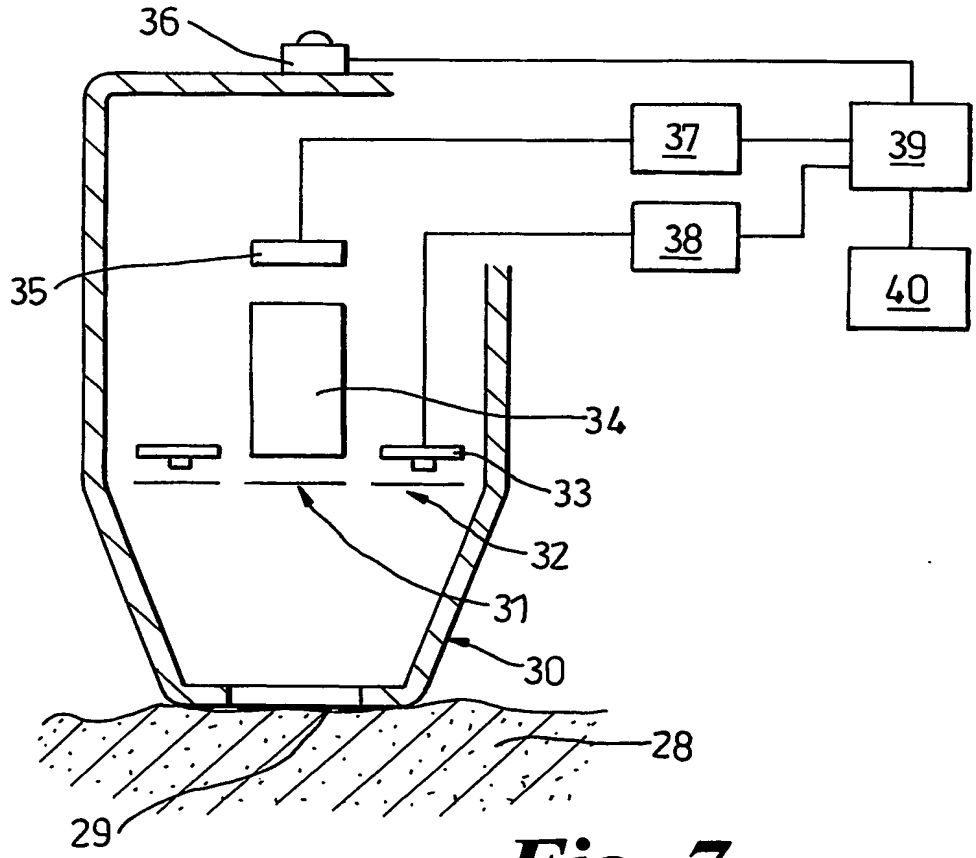

Fig. 7

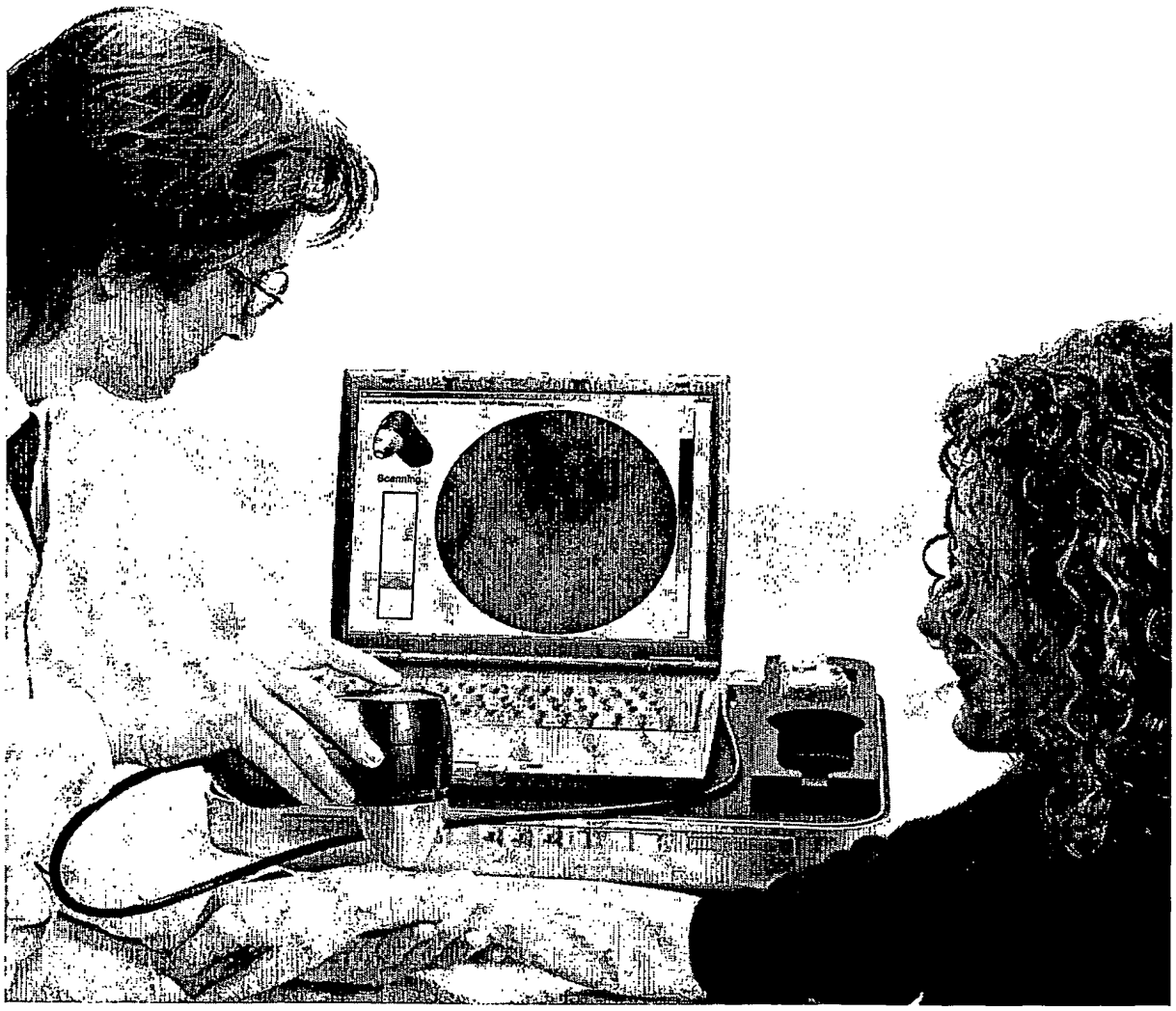

Fig. 8

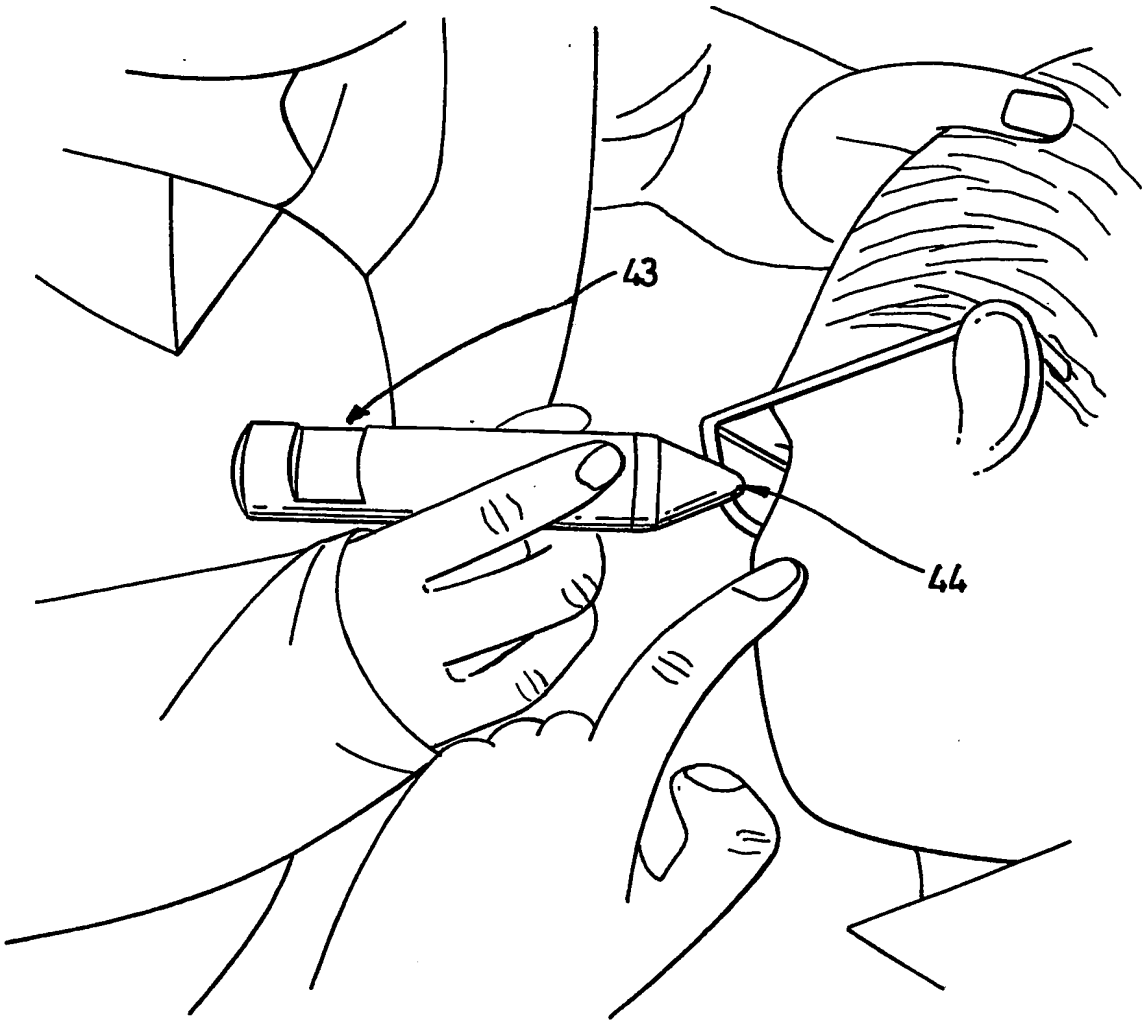

Fig. 9

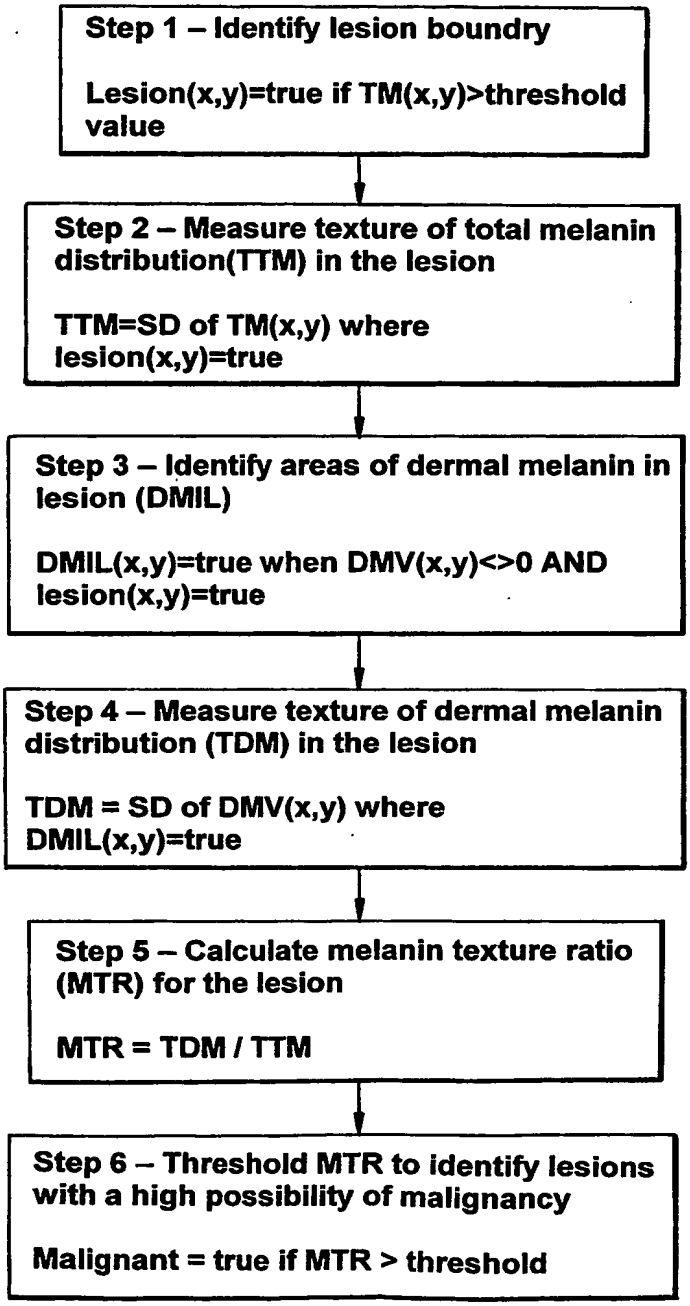
Step 1 – Identify lesion boundry
Lesion(x,y)=true if TM(x,y)>threshold value
Step 2 – Measure texture of total melanin distribution(TTM) in the lesion
TTM=SD of TM(x,y) where lesion(x,y)=true
Step 3 – Identify areas of dermal melanin in lesion (DMIL)
DMIL(x,y)=true when DMV(x,y)<>0 AND lesion(x,y)=true
Step 4 – Measure texture of dermal melanin distribution (TDM) in the lesion
TDM = SD of DMV(x,y) where DMIL(x,y)=true
Step 5 – Calculate melanin texture ratio (MTR) for the lesion
MTR = TDM / TTM
Step 6 – Threshold MTR to identify lesions with a high possibility of malignancy
Malignant = true if MTR > threshold

Fig. 10

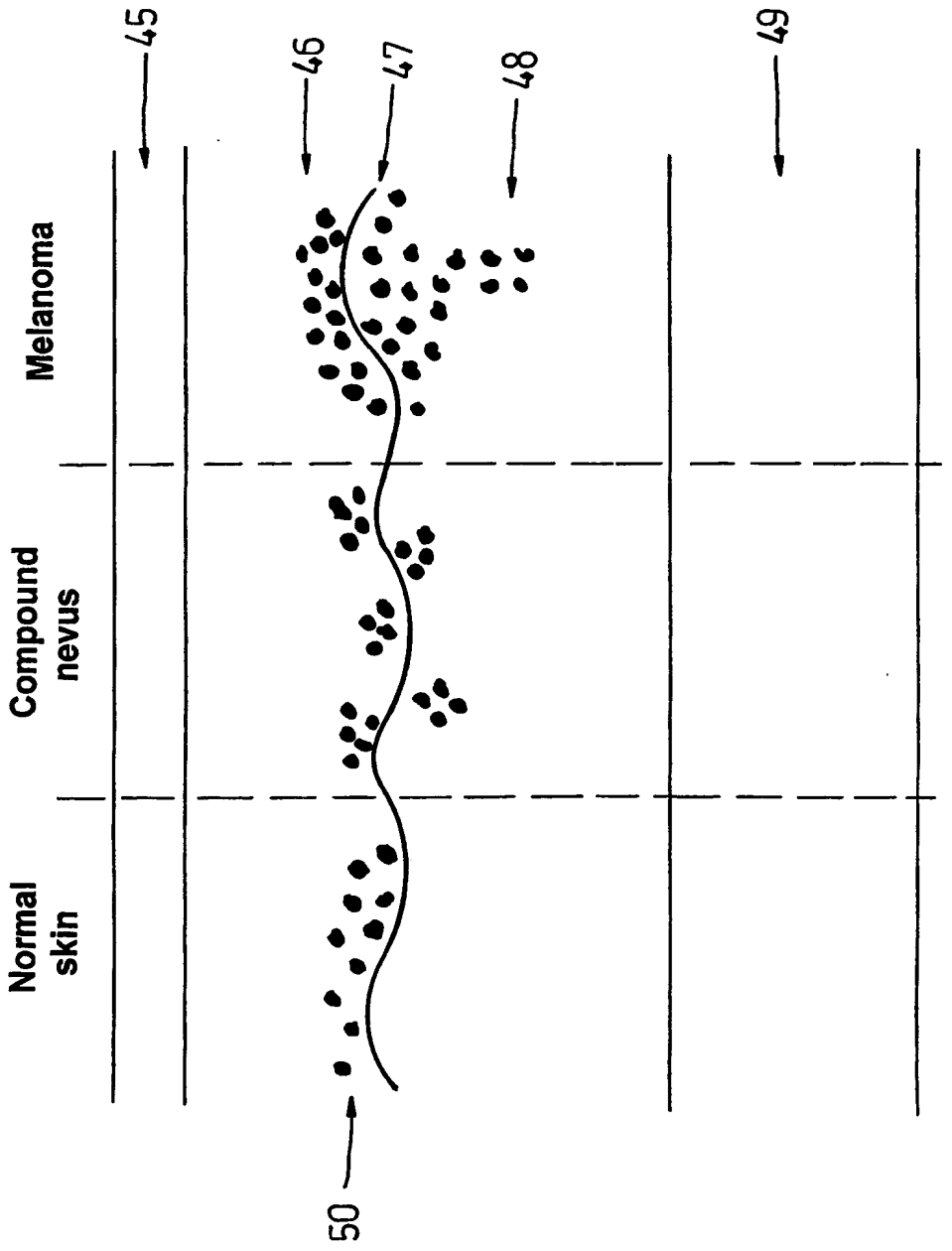

Fig. 11

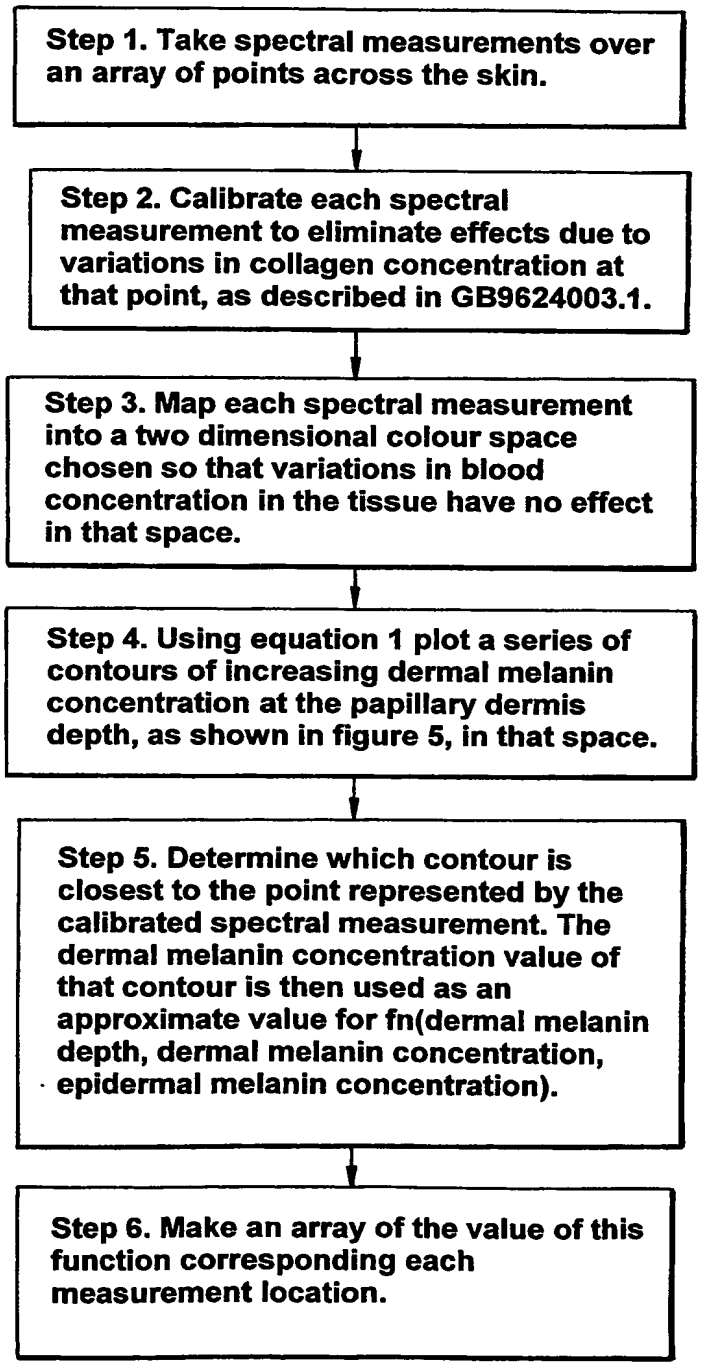
Step 1. Take spectral measurements over an array of points across the skin.
Step 2. Calibrate each spectral measurement to eliminate effects due to variations in collagen concentration at that point, as described in GB9624003.1.
Step 3. Map each spectral measurement into a two dimensional colour space chosen so that variations in blood concentration in the tissue have no effect in that space.
Step 4. Using equation 1 plot a series of contours of increasing dermal melanin concentration at the papillary dermis depth, as shown in figure 5, in that space.
Step 5. Determine which contour is closest to the point represented by the calibrated spectral measurement. The dermal melanin concentration value of that contour is then used as an approximate value for fn(dermal melanin depth, dermal melanin concentration, epidermal melanin concentration).
Step 6. Make an array of the value of this function corresponding each measurement location.

Fig. 12